

31. The nucleic acid according to claim 30, wherein the gene is a gene derived from yeast.

32. The nucleic acid according to claim 30, wherein codon usage of the base sequence is modified to increase a preferred codon of the plant.

33. The nucleic acid according to claim 30, wherein the base sequence is optimized such that G+C content is consistent throughout the entire sequence, without altering the amino acid sequence.

34. The nucleic acid according to claim 30, wherein the base sequence is optimized such that ATTTA sequences are eliminated, without altering the amino acid sequence.

35. The nucleic acid according to claim 30, wherein the base sequence located upstream of the gene's initiation codon is altered to a sequence for effective translation of mRNA known as Kozak sequence.

36. The nucleic acid according to claims 30-35, wherein the nucleic acid is DNA.

37. The DNA according to claim 36, wherein the gene is DNA encoding ferric-chelate reductase FRE1.

38. The DNA according to claim 37, wherein the DNA has a base sequence of SEQ ID NO:1.

39. A nucleic acid having a modified base sequence of a ferric-chelate reductase gene derived from yeast, wherein the sequence is modified by features (A) and (B) without altering the amino acid sequence, for eliminating sequences relating to poly(A) addition, and for

introducing said gene into a plant, wherein features (A) and (B) are defined as follows:

- (A) GT rich regions comprising 8 or more consecutive bases of G or T are eliminated,
and
- (B) sequences encoded by AATAAA, NATAAA, ANTAAA, AANAAA, AATNAA,
AATANA, or AATAAN are eliminated.

40. The nucleic acid according to claim 39, wherein the codon usage of the base sequence is modified to increase a preferred codon of the plant.

41. The nucleic acid according to claim 39, wherein the base sequence is optimized such that G+C content is consistent throughout the entire sequence, without altering the amino acid sequence.

42. The nucleic acid according to claim 39, wherein the base sequence is optimized such that ATTTA sequences are eliminated, without altering the amino acid sequence.

43. The nucleic acid according to claim 39, wherein the base sequence located upstream of the gene's initiation codon is altered to a sequence for effective translation of mRNA known as Kozak sequence.

44. The nucleic acid according to claims 39-43, wherein the nucleic acid is DNA.

45. The DNA according to claim 44, wherein the DNA has a base sequence of SEQ ID NO:1.

REMARKS

Claims 1-16 and 22-29 have been cancelled and new claims 30-45 have been added. It is noted that claims 1-16 were directed to a non-elected invention. No new matter has been added by virtue of these amendments; support therefore being found throughout the specification